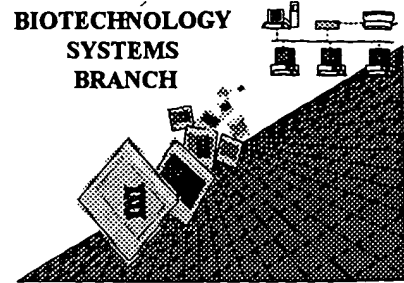


Stolk

RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/234028A
Art Unit / Team No. : 1652
Date Processed by STIC: 5/25/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/234,028A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please d not use "Copy to Disk" function of PatentIn versi n 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/234,028A

DATE: 05/25/1999
TIME: 14:14:43

Input Set: I234028A.RAW

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

E--> 1 <110>
E--> 2 <120>
W--> 3 <130>
4 <140> US/09/234,028A
5 <141> 1999-01-20
E--> 6 <160>

*> see item 13 on Error Summary sheet
for explanation of missing mandatory
items, if file was created
in Patent In 2.0*

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES FOLLOW

E--> 7 <210> 2
8 <211> 456
9 <212> PRT
10 <213> Sus sp.
11 <400> 2
12 Met Asn Leu Asp Ile His Cys Glu Gln Leu Ser Asp Ala Arg Trp Thr
13 1 5 10 15
14 Glu Leu Leu Pro Leu Leu Gln Gln Tyr Glu Val Val Arg Leu Asp Asp
15 20 25 30
16 Cys Gly Leu Thr Glu Glu His Cys Lys Asp Ile Gly Ser Ala Leu Arg
17 35 40 45
18 Ala Asn Pro Ser Leu Thr Glu Leu Cys Leu Arg Thr Asn Glu Leu Gly
19 50 55 60
20 Asp Ala Gly Val His Leu Val Leu Gln Gly Leu Gln Ser Pro Thr Cys
21 65 70 75 80
22 Lys Ile Gln Lys Leu Ser Leu Gln Asn Cys Ser Leu Thr Glu Ala Gly
23 85 90 95
24 Cys Gly Val Leu Pro Ser Thr Leu Arg Ser Leu Pro Thr Leu Arg Glu
25 100 105 110
26 Leu His Leu Ser Asp Asn Pro Leu Gly Asp Ala Gly Leu Arg Leu Leu
27 115 120 125
28 Cys Glu Gly Leu Leu Asp Pro Gln Cys His Leu Glu Lys Leu Gln Leu
29 130 135 140
30 Glu Tyr Cys Arg Leu Thr Ala Ala Ser Cys Glu Pro Leu Ala Ser Val
31 145 150 155 160
32 Leu Arg Ala Thr Arg Ala Leu Lys Glu Leu Thr Val Ser Asn Asn Asp
33 165 170 175
34 Ile Gly Glu Ala Gly Ala Arg Val Leu Gly Gln Gly Leu Ala Asp Ser
35 180 185 190
36 Ala Cys Gln Leu Glu Thr Leu Arg Leu Glu Asn Cys Gly Leu Thr Pro
37 195 200 205
38 Ala Asn Cys Lys Asp Leu Cys Gly Ile Val Ala Ser Gln Ala Ser Leu
39 210 215 220

See next page for explanation of error

FYI
✓

Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

(2107) 1 - Please insert ~~delete - not used~~ *new sequence Rules*
 (2117) ~~SEQUENCE LISTING~~
 <212> PRT *then mandatory*
 <213> Rattus sp. *remove identifier and their responses*

<400> 1

Met Ser Leu Asp Ile Gln Cys Glu Gln Leu Ser Asp Ala Arg Trp Thr
 1 5 10 15

Glu Leu Leu Pro Leu Ile Gln Gln Tyr Gln Val Val Arg Leu Asp Asp
 20 25 30

Cys Gly Leu Thr Glu Val Arg Cys Lys Asp Ile Arg Ser Ala Ile Gln
 35 40 45

Ala Asn Pro Ala Leu Thr Glu Leu Ser Leu Arg Thr Asn Glu Leu Gly
 50 55 60

Asp Ala Gly Val Gly Leu Val Leu Gln Gly Leu Gln Asn Pro Thr Cys
 65 70 75 80

Lys Ile Gln Lys Leu Ser Leu Gln Asn Cys Ser Leu Thr Glu Ala Gly
 85 90 95

Cys Gly Val Leu Pro Asp Val Leu Arg Ser Leu Ser Thr Leu Arg Glu
 100 105 110

Leu His Leu Asn Asp Asn Pro Leu Gly Asp Glu Gly Leu Lys Leu Leu
 115 120 125

Cys Glu Gly Leu Arg Asp Pro Gln Cys Arg Leu Glu Lys Leu Gln Leu
 130 135 140

Glu Tyr Cys Asn Leu Thr Ala Thr Ser Cys Glu Pro Leu Ala Ser Val
 145 150 155 160

Leu Arg Val Lys Pro Asp Phe Lys Glu Leu Val Leu Ser Asn Asn Asp
 165 170 175

Phe His Glu Ala Gly Ile His Thr Leu Cys Gln Gly Leu Lys Asp Ser
 180 185 190

Ala Cys Gln Leu Glu Ser Leu Lys Leu Glu Asn Cys Gly Ile Thr Ser
 195 200 205

Ala Asn Cys Lys Asp Leu Cys Asp Val Val Ala Ser Lys Ala Ser Leu
 210 215 220

Gln Glu Leu Asp Leu Gly Ser Asn Lys Leu Gly Asn Thr Gly Ile Ala
 225 230 235 240

Ala Leu Cys Ser Gly Leu Leu Leu Pro Ser Cys Arg Leu Arg Thr Leu
 245 250 255

Trp Leu Trp Asp Cys Asp Val Thr Ala Glu Gly Cys Lys Asp Leu Cys
 260 265 270

Arg Val Leu Arg Ala Lys Gln Ser Leu Lys Glu Leu Ser Leu Ala Gly
 275 280 285

Asn Glu Leu Lys Asp Glu Gly Ala Gln Leu Leu Cys Glu Ser Leu Leu

290

295

300

Glu Pro Gly Cys Gln Leu Glu Ser Leu Trp Val Lys Thr Cys Ser Leu
305 310 315 320

Thr Ala Ala Ser Cys Pro His Phe Cys Ser Val Leu Thr Lys Asn Ser
325 330 335

Ser Leu Phe Glu Leu Gln Met Ser Ser Asn Pro Leu Gly Asp Ser Gly
340 345 350

Val Val Glu Leu Cys Lys Ala Leu Gly Tyr Pro Asp Thr Val Leu Arg
355 360 365

Val Leu Trp Leu Gly Asp Cys Asp Val Thr Asp Ser Gly Cys Ser Ser
370 375 380

Leu Ala Thr Val Leu Leu Ala Asn Arg Ser Leu Arg Glu Leu Asp Leu
385 390 395 400

Ser Asn Asn Cys Met Gly Asp Asn Gly Val Leu Gln Leu Leu Glu Ser
405 410 415

Leu Lys Gln Pro Ser Cys Ile Leu Gln Gln Leu Val Leu Tyr Asp Ile
420 425 430

Tyr Trp Thr Asp Glu Val Glu Asp Gln Leu Arg Ala Leu Glu Glu Glu
435 440 445

Arg Pro Ser Leu Arg Ile Ile Ser
450 455